



SEQUENCE LISTING

Hanley-Bowdoin, Linda
Orozco, Beverly M.
Gruissem, Wilhelm

<120> GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

<130> 5051.458IP

<140> US 10/633,850

<141> 2003-08-04

<150> US 09/289,346

<151> 1999-04-09

<150> US 60/125,004

<151> 1999-03-18

<160> 113

<170> PatentIn version 3.3

<210> 1

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Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
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<223> Wild-type TGMV AL1 amino acids 111-180

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Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
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50 55 60

Asp Lys Thr Pro Glu Pro
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<223> RS-R125 (Ala1) mutation

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Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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<223> E--N140 + KEE146 (Ala4+5) mutation

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Ser Ala Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

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Asp Lys Thr Pro Glu Pro
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<223> REK154 (Ala6) mutation

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Ser Lys Glu Glu Ala Leu Gln Ile Ile Ala Ala Ala Ile Pro Glu Lys
35 40 45

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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala
35 40 45

Ala Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe

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Asp Lys Thr Pro Glu Pro
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<223> FQ118 (Ala13) mutation

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20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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<223> D120 (Ala14) mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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<223> AAA136 (Leu) mutation

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20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
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Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Gly Cys Ala Ala Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Ala Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
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Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
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<223> KEE146 (Ala5) mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Ala Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
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Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Ala Thr Pro Ala Pro
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5

10

15

Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
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Ser Ala Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

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50 55 60

Asp Lys Thr Pro Glu Pro
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<223> L148 mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
65 70

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20 25 30

Ser Lys Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
65 70

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20 25 30

Ser Lys Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
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<223> III151 mutation

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Ser Lys Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys
35 40 45

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<400> 33
ttctgggatt gcggccgcaa ttatctgcag gg 32

<210> 34
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<223> TGMV AL1 coding sequence

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gtcatcgatg atgtcacacc gcaatatcta aagttgaaac attggaaaga actcattggg 840
gcccaaagag attggcagac taactgtaaa tacggaaagc cagttcaaatt taaaggaggt 900
atcccgtcaa tcgtgctgtc caatcctgga gagggtgcta gctataaagt tttcctcgac 960
aaagagggaaa acactccact aaagaactgg actttccata atgcgaaatt cgtcttcctc 1020
aactcccccc tctatcaaag ctcaacacag agcagc 1056

<210> 51
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

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<220>

<221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 FQ118 mutant (Ala13)

<400> 51		
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt		48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe		
1 5 10 15		
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa		96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln		
20 25 30		
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc		144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys		
35 40 45		
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag		192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln		
50 55 60		
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta		240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val		
65 70 75 80		
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa		288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys		
85 90 95		
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt		336
Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu		
100 105 110		
gta tgg gga gaa gcc gcg gtc gac ggt cga agt gct aga gga ggt tgc		384
Val Trp Gly Glu Ala Ala Val Asp Gly Arg Ser Ala Arg Gly Gly Cys		
115 120 125		
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa		432
Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys		
130 135 140		
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta		480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu		
145 150 155 160		
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag		528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys		
165 170 175		
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac		576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn		
180 185 190		
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt		624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser		
195 200 205		

tcc gct gcg cg	ccg gag aga cct att agt att atc atc gag ggc gat	672	
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp			
210	215	220	
agt cg	acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720	
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			
225	230	235	240
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768		
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys			
245	250	255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816		
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu			
260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864		
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912		
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960		
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008		
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
325	330	335	
tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056		
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	

<210> 52
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 52

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln

50

55

60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Ala Ala Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 53
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)...(1056)
<223> TGMV ALL D120 (Ala14) mutant

<400> 53
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

gta tgg gga gaa gcc gcg gtc gcc ggc cga agt gct aga gga ggt tgc Val Trp Gly Glu Ala Ala Val Ala Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140	432
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Ile Pro Ser Ile 290 295 300	912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305 310 315 320	960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325 330 335	1008

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 54
<211> 352
<212> PRT
<213> Tomato golden mosaic virus

<400> 54

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Ala Ala Val Ala Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn

180

185

190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 55
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 RS-R125 (Ala1) mutant

<400> 55
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe

48

1	5	10	15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	20	25	30	96
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	35	40	45	144
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	50	55	60	192
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	65	70	75	240
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	85	90	95	288
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	100	105	110	336
gta tgg gga gaa ttc cag gtc gac ggt gcg gcc gct gca gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Ala Ala Ala Gly Gly Cys	115	120	125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	130	135	140	432
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	145	150	155	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	165	170	175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	180	185	190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	195	200	205	624
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	210	215	220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	225	230	235	720
				240

tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile 290 295 300	912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305 310 315 320	960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325 330 335	1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser 340 345 350	1056

<210> 56
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 56

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Ala Ala Ala Ala Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp

305

310

315

320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 57
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 QT130 (Ala2) mutant

<400> 57
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

gca gct agc aac gac gct gca gag gcg tta aat gct tct tcc aaa 432
 Ala Ala Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys

130	135	140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta			480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu			
145	150	155	160
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag			528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys			
165	170	175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac			576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn			
180	185	190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt			624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser			
195	200	205	
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat			672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp			
210	215	220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat			720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			
225	230	235	240
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag			768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys			
245	250	255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg			816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu			
260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac			864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc			912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac			960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa			1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
325	330	335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc			1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	

<210> 58
<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 58

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Ala Ala Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 59
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 ND133 (Ala3) mutant

<400> 59
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144

Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	
35							40						45			
aga	gag	ctt	cat	gaa	gat	ggg	caa	cct	cac	ctc	cac	gtg	ctt	att	cag	192
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln	
50							55						60			
ttc	gag	gga	aaa	tac	tgc	tgc	caa	aat	caa	cga	ttc	ttc	gac	ctg	gta	240
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val	
65							70			75			80			
tcc	cca	aca	agg	tca	gca	cat	ttc	cat	cca	aac	att	cag	aga	gct	aaa	288
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys	
85							90			95						
tcg	tct	tcc	gac	gtc	aag	acg	tac	atc	gac	aaa	gac	gga	gat	act	ctt	336
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu	
100							105						110			
gta	tgg	gga	gaa	ttc	cag	gtc	gac	ggt	cga	agt	gct	aga	gga	ggt	tgc	384
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys	
115							120			125						
caa	aca	tct	gcg	gcc	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa	432
Gln	Thr	Ser	Ala	Ala	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys	
130							135			140						
gaa	gaa	gcc	ctg	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta	480
Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	
145							150			155			160			
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
165							170						175			
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
180							185			190						
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
195							200			205						
tcc	gct	gcg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat		672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
210							215			220						
agt	cg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225							230			235			240			
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
245							250			255						
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	

	260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	275	280	285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	290	295	300	912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	305	310	315	960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	325	330	335	1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	340	345	350	1056
<210> 60				
<211> 352				
<212> PRT				
<213> Tomato golden mosaic virus				
<400> 60				
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	1	5	10	15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	20	25	30	
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	35	40	45	
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	50	55	60	
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	65	70	75	80
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	85	90	95	
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	100	105	110	

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Ala Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 61
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 E--N140 (Ala4) mutant

<400> 61
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

caa aca tct aac gac gct gca gcg gcc gcg tta gct gct tct tcc aaa 432
Gln Thr Ser Asn Asp Ala Ala Ala Ala Leu Ala Ala Ser Ser Lys
130 135 140

gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528

Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
165															175	
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
180															190	
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
195															205	
tcc	gct	gcg	ccg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
210															220	
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225															240	
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
245															255	
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
260															270	
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
275															285	
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
290															300	
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305															320	
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
325															335	
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
340															350	

<210> 62
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 62

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Ala Leu Ala Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 63
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 KEE146 (Ala5) mutant

<400> 63
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80	240
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95	288
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu 100 105 110	336
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc gcg Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala 130 135 140	432
gcc gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912

Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
290																
															300	
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305																320
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
325															335	
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
340															350	
<210> 64																
<211> 352																
<212> PRT																
<213> Tomato golden mosaic virus																
<400> 64																
Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe	
1					5				10				15			
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln	
					20			25					30			
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	
					35			40					45			
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln	
					50			55					60			
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val	
					65			70			75		80			
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys	
					85			90					95			
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu	
				100				105					110			
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys	
					115			120					125			
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Ala		
					130			135					140			

Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 65
<211> 1056
<212> DNA

<213> Tomato golden mosaic virus

<220>

<221> CDS

<222> (1)..(1056)

<223> TGMV AL1 REK154 (Ala6) mutant

<400> 65

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

gaa gaa gcc ctg cag ata att gcg gcc gca atc cca gaa aaa tat tta 480
Glu Glu Ala Leu Gln Ile Ile Ala Ala Ile Pro Glu Lys Tyr Leu
145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac 576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt		624	
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser			
195	200	205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat		672	
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp			
210	215	220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat		720	
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			
225	230	235	240
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag		768	
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys			
245	250	255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg		816	
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu			
260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac		864	
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc		912	
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Ile Pro Ser Ile			
290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac		960	
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa		1008	
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
325	330	335	
tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc		1056	
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	

<210> 66
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 66

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys

35

40

45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Ala Ala Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 67
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 EKY159 (Ala7) mutant

<400> 67
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gcg gcc gct tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala Ala Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg ccg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008		
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
325	330	335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056		
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	
<210> 68			
<211> 352			
<212> PRT			
<213> Tomato golden mosaic virus			
<400> 68			
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe			
1	5	10	15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln			
20	25	30	
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys			
35	40	45	
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln			
50	55	60	
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val			
65	70	75	80
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys			
85	90	95	
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu			
100	105	110	
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys			
115	120	125	
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys			
130	135	140	
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala Ala Leu			
145	150	155	160
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys			

165

170

175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 69
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 Q-HN165 (Ala8) mutant

<400> 69

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt gcg ttc gcc gct cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp	
210 215 220	

agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	ctg	ggc	cca	cat	aat	720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225						230				235					240	
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
245						250				255						
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	ctg	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
260						265				270						
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
275						280				285						
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
290						295				300						
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305						310				315			320			
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
325						330				335						
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
340						345				350						

<210> 70
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 70

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile

290

295

300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 71
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 N-DR172 (Ala9) mutant

<400> 71
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys

115	120	125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130	135	140	432
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145	150	155	480
ttt cag ttc cac aat cta aat agc gcg cta gct gcg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe Asp Lys 165	170	175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180	185	190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195	200	205	624
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210	215	220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225	230	235	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245	250	255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260	265	270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275	280	285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile 290	295	300	912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305	310	315	960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325	330	335	1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser 340	345	350	1056

<210> 72
<211> 352
<212> PRT
<213> Tomato golden mosaic virus

<400> 72

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 73
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 K--E179 (Ala10) mutant

<400> 73
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96

Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln	
20							25						30			
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc															144	
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	
35							40						45			
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag															192	
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln	
50							55						60			
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta															240	
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val	
65							70			75			80			
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa															288	
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys	
85							90						95			
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt															336	
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu	
100							105						110			
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc															384	
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys	
115							120						125			
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa															432	
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys		
130							135						140			
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta															480	
Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	
145							150			155			160			
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat gcg															528	
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Ala	
165							170						175			
act ccg gcg cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac															576	
Thr	Pro	Ala	Pro	Trp	Leu	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn		
180							185						190			
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt															624	
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
195							200						205			
tcc gct gcg ccg ccg gag aga cct att agt att atc atc gag ggc gat															672	
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Glu	Gly	Asp		
210							215						220			
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat															720	
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225							230			235			240			
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag															768	
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
225																

	245	250	255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp .Asp Val Thr Pro Gln Tyr Leu Lys Leu	260	265	270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	275	280	285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Ile Pro Ser Ile	290	295	300	912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	305	310	315	960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	325	330	335	1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	340	345	350	1056
<210> 74				
<211> 352				
<212> PRT				
<213> Tomato golden mosaic virus				
<400> 74				
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe 1 5 10 15				
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln 20 25 30				
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys 35 40 45				
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln 50 55 60				
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80				
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95				

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Ala
165 170 175

Thr Pro Ala Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 75
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 AAA136 (Leu) mutant

<400> 75
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

caa aca tct aac gac ctt cta cta gag gcc tta aat gct tct tcc aaa 432
Gln Thr Ser Asn Asp Leu Leu Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480

Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	
145					150				155				160			
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
165						170						175				
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
180						185						190				
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
195						200						205				
tcc	gct	gcg	ccg	ccg	gag	aga	cgt	att	agt	att	atc	atc	gag	ggc	gat	672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
210					215						220					
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	ggc	cca	cat	aat	720	
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225					230					235			240			
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
245					250					255						
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
260					265					270						
aaa	cat	tgg	aaa	gaa	cca	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn		
275					280					285						
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
290					295					300						
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310					315			320			
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
325						330					335					
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
340						345					350					

<210> 76
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 76

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Leu Leu Leu Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 77
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV ALL E--N140 + KEE146 (Ala4+5) mutant

<400> 77
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys 144
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	50	55	60	192	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	65	70	75	80	240
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	85	90	95	288	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	100	105	110	336	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	115	120	125	384	
caa aca tct aac gac gct gca gcg gcc gcg tta gct gct tct tcc gcg Gln Thr Ser Asn Asp Ala Ala Ala Ala Leu Ala Ala Ser Ser Ala	130	135	140	432	
gcc gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	145	150	155	160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	165	170	175	528	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	180	185	190	576	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	195	200	205	624	
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp	210	215	220	672	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	225	230	235	240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	245	250	255	768	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	260	265	270	816	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac				864	

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc			912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac			960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa			1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
325	330	335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc			1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	
<210> 78			
<211> 352			
<212> PRT			
<213> Tomato golden mosaic virus			
<400> 78			
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe			
1	5	10	15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln			
20	25	30	
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys			
35	40	45	
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln			
50	55	60	
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val			
65	70	75	80
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys			
85	90	95	
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu			
100	105	110	
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys			
115	120	125	

Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser Ser Ala
130 135 140

Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 79
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 K144 mutant

<400> 79		
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt		48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe		
1 5 10 15		
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa		96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln		
20 25 30		
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc		144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys		
35 40 45		
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag		192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln		
50 55 60		
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta		240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val		
65 70 75 80		
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa		288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys		
85 90 95		
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt		336
Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu		
100 105 110		
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc		384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys		
115 120 125		
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc gcg		432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala		
130 135 140		
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta		480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu		
145 150 155 160		
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag		528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys		
165 170 175		

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576																																																																																		
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn																																																																																			
180	185	190		gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624	Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser		195	200	205		tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat	672	Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp		210	215	220		agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720	Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn		225	230	235	240	tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768	Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys		245	250	255		gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816	Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu		260	265	270		aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864	Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		275	280	285		tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912	Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350	
190																																																																																			
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624																																																																																		
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser																																																																																			
195	200	205		tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat	672	Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp		210	215	220		agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720	Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn		225	230	235	240	tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768	Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys		245	250	255		gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816	Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu		260	265	270		aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864	Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		275	280	285		tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912	Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350									
205																																																																																			
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat	672																																																																																		
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp																																																																																			
210	215	220		agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720	Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn		225	230	235	240	tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768	Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys		245	250	255		gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816	Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu		260	265	270		aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864	Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		275	280	285		tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912	Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																	
220																																																																																			
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720																																																																																		
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn																																																																																			
225	230	235	240	tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768	Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys		245	250	255		gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816	Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu		260	265	270		aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864	Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		275	280	285		tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912	Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																									
235	240																																																																																		
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768																																																																																		
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys																																																																																			
245	250	255		gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816	Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu		260	265	270		aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864	Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		275	280	285		tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912	Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																																	
255																																																																																			
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816																																																																																		
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu																																																																																			
260	265	270		aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864	Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		275	280	285		tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912	Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																																									
270																																																																																			
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864																																																																																		
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn																																																																																			
275	280	285		tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912	Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																																																	
285																																																																																			
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912																																																																																		
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile																																																																																			
290	295	300		gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960	Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																																																									
300																																																																																			
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960																																																																																		
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp																																																																																			
305	310	315	320	aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008	Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																																																																	
315	320																																																																																		
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008																																																																																		
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys																																																																																			
325	330	335		tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056	Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		340	345	350																																																																									
335																																																																																			
tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056																																																																																		
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser																																																																																			
340	345	350																																																																																	
350																																																																																			

<210> 80
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 80

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln

20

25

30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val
65					70					75					80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu' Ala Leu Asn Ala Ser Ser Ala
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 81
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 E145 mutant

<400> 81
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95	288
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu 100 105 110	336
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140	432
gca gag gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg cgg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile 290 295 300	912

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	
<210> 82	
<211> 352	
<212> PRT	
<213> Tomato golden mosaic virus	
<400> 82	
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	

145	150	155	160
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys			
165	170	175	
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn			
180	185	190	
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser			
195	200	205	
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp			
210	215	220	
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			
225	230	235	240
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys			
245	250	255	
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu			
260	265	270	
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
275	280	285	
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
290	295	300	
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
305	310	315	320
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
325	330	335	
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	
<210> 83			
<211> 1056			
<212> DNA			
<213> Tomato golden mosaic virus			

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 E146 mutant

<400> 83

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	

tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 84
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 84

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn

275

280

285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 85

<211> 1056

<212> DNA

<213> Tomato golden mosaic virus

<220>

<221> CDS

<222> (1)..(1056)

<223> TGMV AL1 EE146 mutant

<400> 85

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu

100	105	110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aca gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115	120	125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130	135	140	432
gcg gcc gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145	150	155	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165	170	175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180	185	190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195	200	205	624
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210	215	220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225	230	235	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245	250	255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260	265	270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275	280	285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile 290	295	300	912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305	310	315	960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325	330	335	1008

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc			1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	
<210> 86			
<211> 352			
<212> PRT			
<213> Tomato golden mosaic virus			
<400> 86			
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe			
1	5	10	15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln			
20	25	30	
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys			
35	40	45	
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln			
50	55	60	
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val			
65	70	75	80
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys			
85	90	95	
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu			
100	105	110	
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys			
115	120	125	
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys			
130	135	140	
Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu			
145	150	155	160
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys			
165	170	175	

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 87
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV ALL A147Y mutant

<400> 87
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe			
1	5	10	15
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa			96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln			
20	25	30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc			144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys			
35	40	45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag			192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln			
50	55	60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta			240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val			
65	70	75	80
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa			288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys			
85	90	95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt			336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu			
100	105	110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc			384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys			
115	120	125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa			432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys			
130	135	140	
gaa gaa tac ctt cag ata att aga gag aaa atc cca gaa aaa tat tta			480
Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu			
145	150	155	160
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag			528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys			
165	170	175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac			576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn			
180	185	190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt			624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser			
195	200	205	
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat			672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp			
210	215	220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat			720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			

225	230	235	240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255				768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270				816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285				864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Ile Pro Ser Ile 290 295 300				912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305 310 315 320				960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325 330 335				1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser 340 345 350				1056
<p><210> 88 <211> 352 <212> PRT <213> Tomato golden mosaic virus</p> <p><400> 88</p>				
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe 1 5 10 15				
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln 20 25 30				
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys 35 40 45				
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln 50 55 60				
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80				

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 89
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 L148 mutant

<400> 89
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

caa aca tct aac gac gct gca gag gcg tta aat gct tct tcc aaa 432

Gln	Thr	Ser	Asn	Asp	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys	
130					135					140					
gaa gaa gct gcg cag ata att aga gag aaa atc cca gaa aaa tat tta														480	
Glu	Glu	Ala	Ala	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu
145					150				155				160		
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag														528	
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys
					165				170				175		
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac														576	
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn
					180				185				190		
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt														624	
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser
					195				200				205		
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat														672	
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Glu	Gly	Asp	
					210				215				220		
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat														720	
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn
					225				230				240		
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag														768	
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys
					245				250				255		
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg														816	
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu
					260				265				270		
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac														864	
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn
					275				280				285		
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc														912	
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile
					290				295				300		
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac														960	
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp
					305				310				315		
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa														1008	
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys
					325				330				335		
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc														1056	
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser
					340				345				350		

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 90

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 91
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 L148V mutant

<400> 91
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys 35 40 45	144
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln 50 55 60	192
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80	240
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95	288
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu 100 105 110	336
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140	432
gaa gag gcc gtg cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816

Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
260								265					270			
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
275							280					285				
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
290							295					300				
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310						315			320		
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
325							330					335				
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
340							345					350				
<210> 92																
<211> 352																
<212> PRT																
<213> Tomato golden mosaic virus																
<400> 92																
Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe	
1					5				10				15			
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln	
					20			25					30			
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	
					35			40					45			
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln	
					50			55					60			
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val	
					65			70			75			80		
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys	
					85			90					95			
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu	
					100			105					110			

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 93
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 L148V* mutant

<400> 93
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432
 Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

gaa gaa gcc gtt cag ata att aga gag aaa atc cca gaa aaa tat tta 480
 Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285	864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile 290 295 300	912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305 310 315 320	960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325 330 335	1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser 340 345 350	1056

<210> 94
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

 <400> 94

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe

1

5

10

15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 95
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 L148G mutant

<400> 95
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80	240
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95	288
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu 100 105 110	336
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140	432
gaa gaa gcc ggc cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270	816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285	864

tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912		
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960		
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008		
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
325	330	335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056		
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
340	345	350	

<210> 96

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 96

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe			
1	5	10	15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln		
20	25	30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys		
35	40	45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln		
50	55	60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val			
65	70	75	80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys		
85	90	95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu		
100	105	110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys		
115	120	125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys

130

135

140

Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 97
<211> 1056

<212> DNA

<213> Tomato golden mosaic virus

<220>

<221> CDS

<222> (1)..(1056)

<223> TGMV AL1 II151 mutant

<400> 97

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

gaa gaa gcc ctt cag gca gct aga gag aaa atc cca gaa aaa tat tta 480
Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac 576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
tcc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 98
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 98

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu

260

265

270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 99
<211> 25
<212> PRT
<213> Tomato golden mosaic virus

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> Amino acids 132-156 of TGMV AL1

<400> 99

Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys Glu Glu Ala
1 5 10 15

Leu Gln Ile Ile Arg Glu Lys Ile Pro
20 25

<210> 100
<211> 13
<212> PRT
<213> Tomato golden mosaic virus

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> TGMV AL1 amino acids 144-156

<400> 100

Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro
1 5 10

<210> 101
<211> 13
<212> PRT
<213> tomato yellow leaf curl virus

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> TYLCV C1 amino acids 142-154

<400> 101

Lys Ser Glu Ala Leu Lys Ile Leu Arg Glu Leu Ala Pro
1 5 10

<210> 102
<211> 13
<212> PRT
<213> cabbage leaf curl virus

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CbLCV AL1 amino acids 141-153

<400> 102

Val Glu Glu Ala Leu Ala Ile Ile Arg Ala Gly Asp Pro
1 5 10

<210> 103
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide primer

<400> 103
ggacaccgat tggatccagc atgcctc

27

<210> 104
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide primer

<400> 104	ccacagtcga attccccggg cttacgc	27
<210> 105		
<211> 36		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Mutagenesis oligonucleotide		
<400> 105	cctaaataaag atctacaagg atcccacgaa acccta	36
<210> 106		
<211> 31		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> CbLCV AL1 L145A mutagenesis oligonucleotide		
<400> 106	gtgtggaaga ggcggccgca attataaggg c	31
<210> 107		
<211> 349		
<212> PRT		
<213> cabbage leaf curl virus		
<400> 107		
Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe		
1 5 10 15		
Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met		
20 25 30		
Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val		
35 40 45		
Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile		
50 55 60		
Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile		
65 70 75 80		
Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala		

85

90

95

Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr
100 105 110

Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys
115 120 125

Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala
130 135 140

Leu Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr
145 150 155 160

His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu
165 170 175

Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp
180 185 190

Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala
195 200 205

Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr
210 215 220

Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser
225 230 235 240

Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr
245 250 255

Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp
260 265 270

Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr
275 280 285

Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys
290 295 300

Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu
305 310 315 320

Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr
325 330 335

Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys
340 345

<210> 108
<211> 70
<212> PRT
<213> cabbage leaf curl virus

<220>
<221> MISC_FEATURE
<222> (1)..(70)
<223> Wild-type CbLCV ALL amino acids 111-180

<400> 108

Asp Tyr Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala
1 5 10 15

Asn Lys Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu
20 25 30

Glu Ala Leu Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val
35 40 45

Ser Tyr His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala
50 55 60

Pro Glu Pro Trp Ala Pro
65 70

<210> 109
<211> 70
<212> PRT
<213> cabbage leaf curl virus

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> L145A mutation

<400> 109

Asp Tyr Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala

1

5

10

15

Asn Lys Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu
 20 25 30

Glu Ala Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val
 35 40 45

Ser Tyr His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala
 50 55 60

Pro Glu Pro Trp Ala Pro
 65 70

<210> 110
 <211> 1047
 <212> DNA
 <213> cabbage leaf curl virus

<220>
 <221> misc_feature
 <222> (1)..(1047)
 <223> CbLCV AL1 coding sequence

<400> 110
 atgccacgaa accctaaatc gtttcgttta gcagccgaa atatattctt aacatatccc 60
 cagtgcgaca tacccaaaga tgaagctctt cagatgcttc aaaccctgtc gtggtcagtc 120
 gtcaaaaccca catacatcag agtcgcaaga gaggaacatt cagacgggtt ccccccattta 180
 cactgtctca tccaaactatc aggaaagtctg aacatcaagg atgcttagatt ttgcacatc 240
 actcaccacca gaaggctctgc caatttcac ccaaacattc aggcagccaa agacaccaat 300
 gccgtcaaga attacatcac caaagatggt gattattgtg aatccggca gtacaagggt 360
 tctgggggta caaaggcaaa taaagacgac gtctaccaca acgccgtcaa tgcggatgt 420
 gtggaagagg ctctcgcaat tataagggtt ggagatccaa agacgttcat tgtagttat 480
 cataatgtta gagctaacat agagcgactc tttactaagg ctccggaaacc atgggctcct 540
 ccgtttcaac tctccctcatt tactaacgtc ccggacgaga tgagttcatg ggcagatgac 600
 tattttggtc ggagtgccgc tgcgccggcg gaaagaccta ttagtatcat agttgaaggt 660
 gattcacgaa ccggcaagac catgtggcg cgtgctttag gaccacataa ttatggat 720
 gggcacctcg acttaattc aaaggcttt tcaaataatg cgagttataa cgtcattgt 780

gacatagtc cgcatatct aaagctaaag cactggaaag agcttattgg ggcccaaagg	840
gactggcaat caaactgtaa gtacggcaag ccagttcaaa ttcaaagggtgg cataccctca	900
atcgtgctgt gcaatccagg agaggggagc agttatataa gtttcctcaa caaagaggaa	960
aatgcacac taagagcgtg gactacaaa aatgcaaaat tcacactct tgaagcccc	1020
ctctatcaaa gcacagcaca agattgc	1047
<210> 111	
<211> 1047	
<212> DNA	
<213> cabbage leaf curl virus	
<220>	
<221> CDS	
<222> (1)..(1047)	
<223> CbLCV AL1 L145A mutation	
<400> 111	
atg cca cga aac cct aaa tcg ttt cgt tta gca gcc cga aat ata ttc	48
Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe	
1 5 10 15	
tta aca tat ccc cag tgc gac ata ccc aaa gat gaa gct ctt cag atg	96
Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met	
20 25 30	
ctt caa acc ctg tcg tgg tca gtc gtc aaa ccc aca tac atc aga gtc	144
Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val	
35 40 45	
gca aga gag gaa cat tca gac ggg ttc ccc cat tta cac tgt ctc atc	192
Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile	
50 55 60	
caa cta tca gga aag tcg aac atc aag gat gct aga ttt ttc gac atc	240
Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile	
65 70 75 80	
act cac ccc aga agg tct gcc aat ttt cac cca aac att cag gca gcc	288
Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala	
85 90 95	
aaa gac acc aat gcc gtc aag aat tac atc acc aaa gat ggt gat tat	336
Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr	
100 105 110	
tgt gaa tcc ggg cag tac aag gtg tct ggg ggt aca aag gca aat aaa	384
Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys	
115 120 125	
gac gac gtc tac cac aac gcc gtc aat gcg gga tgt gtg gaa gag gcg	432
Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala	

130	135	140	
gcc gca att ata agg gct gga gat cca aag acg ttc att gtt agt tat Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr 145	150	155	480
cat aat gtt aga gct aac ata gag cga ctc ttt act aag gct ccg gaa His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu 165	170	175	528
cca tgg gct cct ccg ttt caa ctc tcc tcc ttt act aac gtc ccg gac Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp 180	185	190	576
gag atg agt tca tgg gca gat gac tat ttt ggt cgg agt gcc gct gcg Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala 195	200	205	624
cgg gcg gaa aga cct att agt atc ata gtt gaa ggt gat tca cga acc Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr 210	215	220	672
ggc aag acc atg tgg gcg cgt gct tta gga cca cat aat tat ttg agt Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser 225	230	235	720
ggg cac ctc gac ttt aat tca aag gtc ttt tca aat aat gcg gag tat Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr 245	250	255	768
aac gtc att gat gac ata gct ccg cat tat cta aag cta aag cac tgg Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp 260	265	270	816
aaa gag ctt att ggg gcc caa agg gac tgg caa tca aac tgt aag tac Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr 275	280	285	864
ggc aag cca gtt caa att aaa ggt ggc ata ccc tca atc gtg ctg tgc Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys 290	295	300	912
aat cca gga gag ggg agc agt tat ata agt ttc ctc aac aaa gag gaa Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu 305	310	315	960
aat gca tca cta aga gcg tgg act acc aaa aat gca aaa ttc atc act Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr 325	330	335	1008
ctt gaa gcc ccc ctc tat caa agc aca gca caa gat tgc Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys 340	345		1047

<210> 112
<211> 349

<212> PRT

<213> cabbage leaf curl virus

<400> 112

Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met
20 25 30

Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val
35 40 45

Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile
50 55 60

Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile
65 70 75 80

Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala
85 90 95

Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr
100 105 110

Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys
115 120 125

Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala
130 135 140

Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr
145 150 155 160

His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu
165 170 175

Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp
180 185 190

Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala
195 200 205

Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr
210 215 220

Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser
225 230 235 240

Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr
245 250 255

Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp
260 265 270

Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr
275 280 285

Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys
290 295 300

Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu
305 310 315 320

Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr
325 330 335

Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys
340 345

<210> 113
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Consensus begomovirus AL1/C1 sequence

<220>
<221> MISC_FEATURE
<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid, but is generally a charged amino acid which is optionally present or absent

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be Leu or Met

<220>

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<221> misc_feature
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa can be Ile or Val

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa can be Ile or Leu

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa can be Arg or Lys

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa can be Glu or Asp

<220>
<221> misc_feature
<222> (11)..(12)
<223> Xaa can be any naturally occurring amino acid

<400> 113
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Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
1 5 10